RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/791,017C
Source: IFW16
Date Processed by STIC: 07/27/2006

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 07/27/2006
PATENT APPLICATION: **US/10/791,017C** TIME: 09:50:25

Input Set : **A:\791017eightsequences.txt**
Output Set: **N:\CRF4\07272006\J791017C.raw**

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      3 <110> APPLICANT: JENAPHARM GmbH & Co. KG
W-->  4 <120> TITLE OF INVENTION: Methods for Determining Hormonal Effects
W-->  5       of Substances
W-->  6 <130> FILE REFERENCE: Pat 3684/11
W-->  7 <140> CURRENT APPLICATION NUMBER: US/10/791,017C
      8 <141> CURRENT FILING DATE: 2004-03-02
W-->  9 <160> NUMBER OF SEQ ID: 8
     10 <170> SOFTWARE: PatentIn Ver. 2.1
W--> 11 <210> SEQ ID NO: 1
     12 <211> LENGTH: 2390
     13 <212> TYPE: DNA
     14 <213> ORGANISM: Homo sapiens
W--> 15 <220> FEATURE:
     16 <221> NAME/KEY: CDS
     17 <222> LOCATION: (44)..(2011)
     18 <223> OTHER INFORMATION: EWS
W--> 19 <400> SEQUENCE: 1
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     21                                                 Met Ala Ser Thr
     22                                                   1
     24 gat tac agt acc tat agc caa gct gca gcg cag cag ggc tac agt gct    103
     25 Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln Gly Tyr Ser Ala
     26   5                  10                  15                  20
     28 tac acc gcc cag ccc act caa gga tat gca cag acc acc cag gca tat    151
     29 Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr Thr Gln Ala Tyr
     30                  25                  30                  35
     32 ggg caa caa agc tat gga acc tat gga cag ccc act gat gtc agc tat    199
     33 Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr Asp Val Ser Tyr
     34              40                  45                  50
     36 acc cag gct cag acc act gca acc tat ggg cag acc gcc tat gca act    247
     37 Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr Ala Tyr Ala Thr
     38          55                  60                  65
     40 tct tat gga cag cct ccc act ggt tat act act cca act gcc ccc cag    295
     41 Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro Thr Ala Pro Gln
     42      70                  75                  80
     44 gca tac agc cag cct gtc cag ggg tat ggc act ggt gct tat gat acc    343
     45 Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly Ala Tyr Asp Thr
     46  85                  90                  95                 100
     48 acc act gct aca gtc acc acc acc cag gcc tcc tat gca gct cag tct    391
     49 Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr Ala Ala Gln Ser
     50                 105                 110                 115
     52 gca tat ggc act cag cct gct tat cca gcc tat ggg cag cag cca gca    439
     53 Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly Gln Gln Pro Ala
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54              120                 125                 130
56 gcc act gca cct aca aga ccg cag gat gga aac aag ccc act gag act    487
57 Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys Pro Thr Glu Thr
58          135                 140                 145
60 agt caa cct caa tct agc aca ggg ggt tac aac cag ccc agc cta gga    535
61 Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln Pro Ser Leu Gly
62      150                 155                 160
64 tat gga cag agt aac tac agt tat ccc cag gta cct ggg agc tac ccc    583
65 Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro Gly Ser Tyr Pro
66 165                 170                 175                 180
68 atg cag cca gtc act gca cct cca tcc tac cct cct acc agc tat tcc    631
69 Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro Thr Ser Tyr Ser
70                 185                 190                 195
72 tct aca cag ccg act agt tat gat cag agc agt tac tct cag cag aac    679
73 Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr Ser Gln Gln Asn
74              200                 205                 210
76 acc tat ggg caa ccg agc agc tat gga cag cag agt agc tat ggt caa    727
77 Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln
78          215                 220                 225
80 caa agc agc tat ggg cag cag cct ccc act agt tac cca ccc caa act    775
81 Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr Pro Pro Gln Thr
82      230                 235                 240
84 gga tcc tac agc caa gct cca agt caa tat agc caa cag agc agc agc    823
85 Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln Ser Ser Ser
86 245                 250                 255                 260
88 tac ggg cag cag agt tca ttc cga cag gac cac ccc agt agc atg ggt    871
89 Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro Ser Ser Met Gly
90                 265                 270                 275
92 gtt tat ggg cag gag tct gga gga ttt tcc gga cca gga gag aac cgg    919
93 Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro Gly Glu Asn Arg
94              280                 285                 290
96 agc atg agt ggc cct gat aac cgg ggc agg gga aga ggg gga ttt gat    967
97 Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg Gly Gly Phe Asp
98          295                 300                 305
100 cgt gga ggc atg agc aga ggt ggg cgg gga gga gga cgc ggt gga atg   1015
101 Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly Arg Gly Gly Met
102     310                 315                 320
104 ggc agc gct gga gag cga ggt ggc ttc aat aag cct ggt gga ccc atg   1063
105 Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly Gly Pro Met
106 325                 330                 335                 340
108 gat gaa gga cca gat ctt gat cta ggc cca cct gta gat cca gat gaa   1111
109 Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val Asp Pro Asp Glu
110                 345                 350                 355
112 gac tct gac aac agt gca att tat gta caa gga tta aat gac agt gtg   1159
113 Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn Asp Ser Val
114             360                 365                 370
117 act cta gat gat ctg gca gac ttc ttt aag cag tgt ggg gtt gtt aag   1207
118 Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly Val Val Lys
119         375                 380                 385
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```
121 atg aac aag aga act ggg caa ccc atg atc cac atc tac ctg gac aag   1255
122 Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr Leu Asp Lys
123     390                 395                 400
125 gaa aca gga aag ccc aaa ggc gat gcc aca gtg tcc tat gaa gac cca   1303
126 Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr Glu Asp Pro
127 405                 410                 415                 420
129 ccc act gcc aag gct gcc gtg gaa tgg ttt gat ggg aaa gat ttt caa   1351
130 Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys Asp Phe Gln
131                 425                 430                 435
133 ggg agc aaa ctt aaa gtc tcc ctt gct cgg aag aag cct cca atg aac   1399
134 Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro Pro Met Asn
135             440                 445                 450
137 agt atg cgg ggt ggt ctg cca ccc cgt gag ggc aga ggc atg cca cca   1447
138 Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg Gly Met Pro Pro
139         455                 460                 465
141 cca ctc cgt gga ggt cca gga ggc cca gga ggt cct ggg gga ccc atg   1495
142 Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Met
143     470                 475                 480
145 ggt cgc atg gga ggc cgt gga gga gat aga gga ggc ttc cct cca aga   1543
146 Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe Pro Pro Arg
147 485                 490                 495                 500
149 gga ccc cgg ggt tcc cga ggg aac ccc tct gga gga gga aac gtc cag   1591
150 Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Gly Asn Val Gln
151                 505                 510                 515
153 cac cga gct gga gac tgg cag tgt ccc aat ccg ggt tgt gga aac cag   1639
154 His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys Gly Asn Gln
155             520                 525                 530
157 aac ttc gcc tgg aga aca gag tgc aac cag tgt aag gcc cca aag cct   1687
158 Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro
159         535                 540                 545
161 gaa ggc ttc ctc ccg cca ccc ttt ccg ccc ccg ggt ggt gat cgt ggc   1735
162 Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly Gly Asp Arg Gly
163     550                 555                 560
165 aga ggt ggc cct ggt ggc atg cgg gga gga aga ggt ggc ctc atg gat   1783
166 Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly Gly Leu Met Asp
167 565                 570                 575                 580
169 cgt ggt ggt ccc ggt gga atg ttc aga ggt ggc cgt ggt gga gac aga   1831
170 Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly Gly Asp Arg
171                 585                 590                 595
173 ggt ggc ttc cgt ggt ggc cgg ggc atg gac cga ggt ggc ttt ggt gga   1879
174 Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly Phe Gly Gly
175             600                 605                 610
177 gga aga cga ggt ggc cct ggg ggg ccc cct gga cct ttg atg gaa cag   1927
178 Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro Leu Met Glu Gln
179         615                 620                 625
181 atg gga gga aga aga gga gga cgt gga gga cct gga aaa atg gat aaa   1975
182 Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly Lys Met Asp Lys
183     630                 635                 640
185 ggc gag cac cgt cag gag cgc aga gat cgg ccc tac tagatgcaga       2021
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Input Set : **A:\791017eightsequences.txt**
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186 Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
187 645                 650                 655
189 gaccccgcag agctgcattg actaccagat ttatttttta aaccagaaaa tgttttaaat 2081
191 ttataattcc atatttataa tgttggccac aacattatga ttattccttg tctgtacttt 2141
193 agtatttttc accatttgtg aagaaacatt aaaacaagtt aaatggtagt gtgcggagtt 2201
195 ttttttttctt ccttctttta aaaatggttg tttaagactt taacaatggg aaccccttgt 2261
197 gagcatgctc agtatcattg tggagaacca agagggcctg ttaactgtaa caatgttcat 2321
199 ggttgtgatg ttttttttttt ttttttaaaa taaaattcca aatgtttaat aaaaaaaaaa 2381
201 aaaaaaaaa                                                        2390
204 <210> SEQ ID NO: 2
205 <211> LENGTH: 656
206 <212> TYPE: PRT
207 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 2
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212   1               5                  10                  15
214 Gly Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr
215              20                  25                  30
217 Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr
218          35                  40                  45
220 Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr
221      50                  55                  60
223 Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro
224  65                  70                  75                  80
226 Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly
227                  85                  90                  95
229 Ala Tyr Asp Thr Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr
230             100                 105                 110
232 Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly
233         115                 120                 125
235 Gln Gln Pro Ala Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys
236     130                 135                 140
238 Pro Thr Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln
239 145                 150                 155                 160
241 Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro
242                 165                 170                 175
244 Gly Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro
245             180                 185                 190
247 Thr Ser Tyr Ser Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr
248         195                 200                 205
250 Ser Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser
251     210                 215                 220
253 Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr
254 225                 230                 235                 240
256 Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln
257                 245                 250                 255
259 Gln Ser Ser Ser Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro
260             260                 265                 270
262 Ser Ser Met Gly Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro
```

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Input Set : **A:\791017eightsequences.txt**
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```
263         275                 280                 285
265 Gly Glu Asn Arg Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg
266     290                 295                 300
268 Gly Gly Phe Asp Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly
269 305                 310                 315                 320
271 Arg Gly Gly Met Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro
272                 325                 330                 335
274 Gly Gly Pro Met Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val
275             340                 345                 350
277 Asp Pro Asp Glu Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu
278         355                 360                 365
280 Asn Asp Ser Val Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys
281     370                 375                 380
283 Gly Val Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile
284 385                 390                 395                 400
286 Tyr Leu Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser
287                 405                 410                 415
289 Tyr Glu Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly
290             420                 425                 430
292 Lys Asp Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys
293         435                 440                 445
295 Pro Pro Met Asn Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg
296     450                 455                 460
298 Gly Met Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro
299 465                 470                 475                 480
301 Gly Gly Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly
302                 485                 490                 495
304 Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
305             500                 505                 510
307 Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly
308         515                 520                 525
310 Cys Gly Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys
311     530                 535                 540
313 Ala Pro Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly
314 545                 550                 555                 560
316 Gly Asp Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly
317                 565                 570                 575
319 Gly Leu Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg
320             580                 585                 590
322 Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly
323         595                 600                 605
325 Gly Phe Gly Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro
326     610                 615                 620
328 Leu Met Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly
329 625                 630                 635                 640
331 Lys Met Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
332                 645                 650                 655
335 <210> SEQ ID NO: 3
336 <211> LENGTH: 20
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VERIFICATION SUMMARY DATE: 07/27/2006
PATENT APPLICATION: **US/10/791,017C** TIME: 09:50:26

Input Set : **A:\791017eightsequences.txt**
Output Set: **N:\CRF4\07272006\J791017C.raw**

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L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:9 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <210> field identifier
L:15 M:283 W: Missing Blank Line separator, <220> field identifier
L:19 M:283 W: Missing Blank Line separator, <400> field identifier